

Quick Start Guide

Overview

This guide gives the basics of Partek® Flow® usage. Partek Flow can be installed in either a server, computer cluster or on the cloud. Regardless of where it's installed, it can be viewed using any web browser. We recommend using Google Chrome.

This guide covers:

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Logging in to your Partek Flow account will bring up the *Home page* (Figure 1). This page will show recent activities you've performed, recent projects you've worked on and pertinent details about each project.

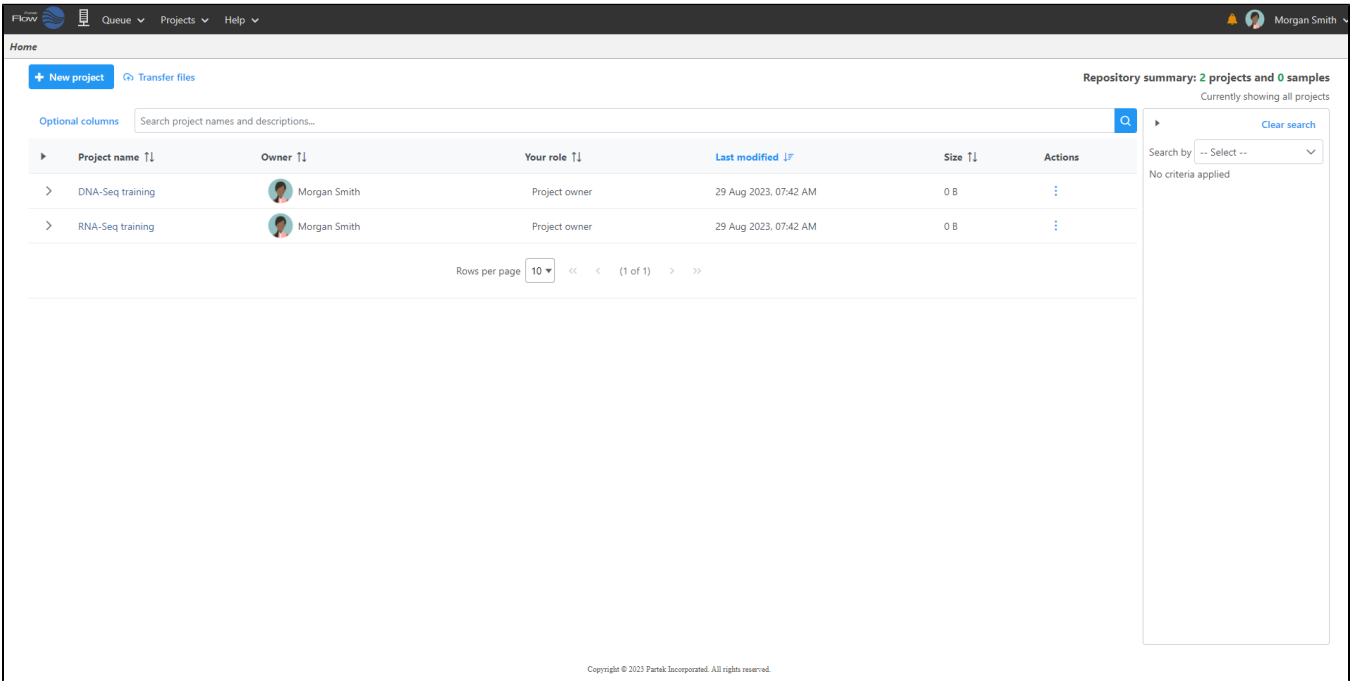
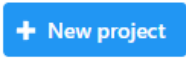


Figure 9. Partek Flow Home page

Starting a new project

From the *Home Page*, click the **New project** button . Assign a name to the project and click the **Create project** button.

Uploading your dataset

Upon creation of a new project, the *Analyses* tab will appear, prompting you to add samples to your project. Click the blue **Add data** button  (Figure 2).

Select the type of data (**Single cell**, **Bulk**, **Other**), choose the **assay** type, and select the data **format**. Partek Flow accepts various data types. Use the **Next** button to proceed with import.

There are three ways you can upload the data:

1. From your Partek Flow server ([click here for more information](#))
2. From a URL
3. From a GEO / ENA Bioproject ([click here for more information](#))

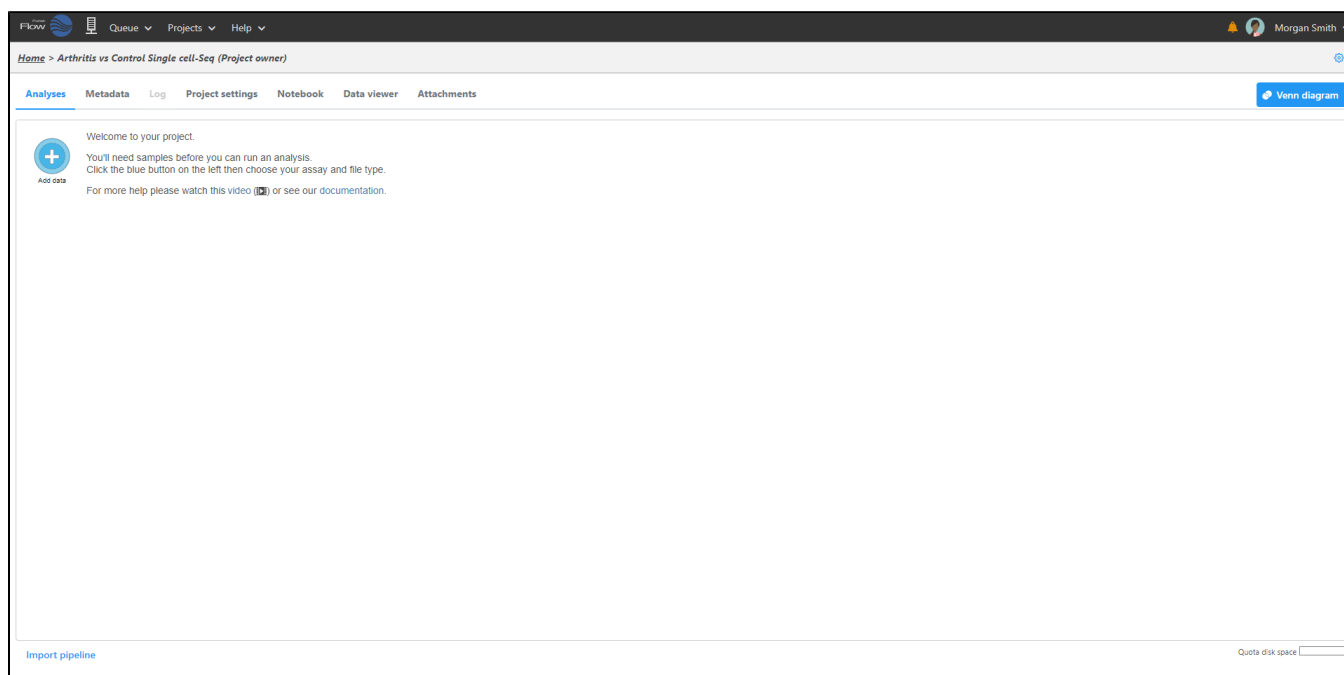


Figure 10. Add data to the project by clicking the blue circle

Because genomics datasets are generally large, it is ideal to have the data copied in a folder directly accessible to the Partek Flow server. Make sure that the directory has the appropriate permissions for Partek Flow to read and write files in that folder. You may wish to seek assistance from your system administrator in uploading your data directly.

Select the files you would like to create samples from. Once they've been created, assign the corresponding sample attributes for each sample using the **Metadata** tab. The most efficient way to assign sample attributes is by clicking **Assign sample attributes from a file** and uploading a tab delimited text file. The file should contain a table with the following:

- The first row lists the attribute names (e.g. Treatment, Exposure) and
- The first column of the table lists the sample names (the sample names in the file must be identical to the ones listed in the *Sample name* column in the *Data* tab)
- List the corresponding attributes for each sample in the succeeding columns

Basic Partek Flow layout

The Analyses Tab

After samples have been added and associated with valid data files, a data node will appear in the *Analyses* tab (Figure 3). The *Analyses* tab is where you can invoke tasks, using the context sensitive menu on the right, and view the results of your analysis.

To add more data use the **Add data** task in the menu on the right or **Add data** in the **Metadata** tab. Once a task is performed, data can no longer be added to the project.

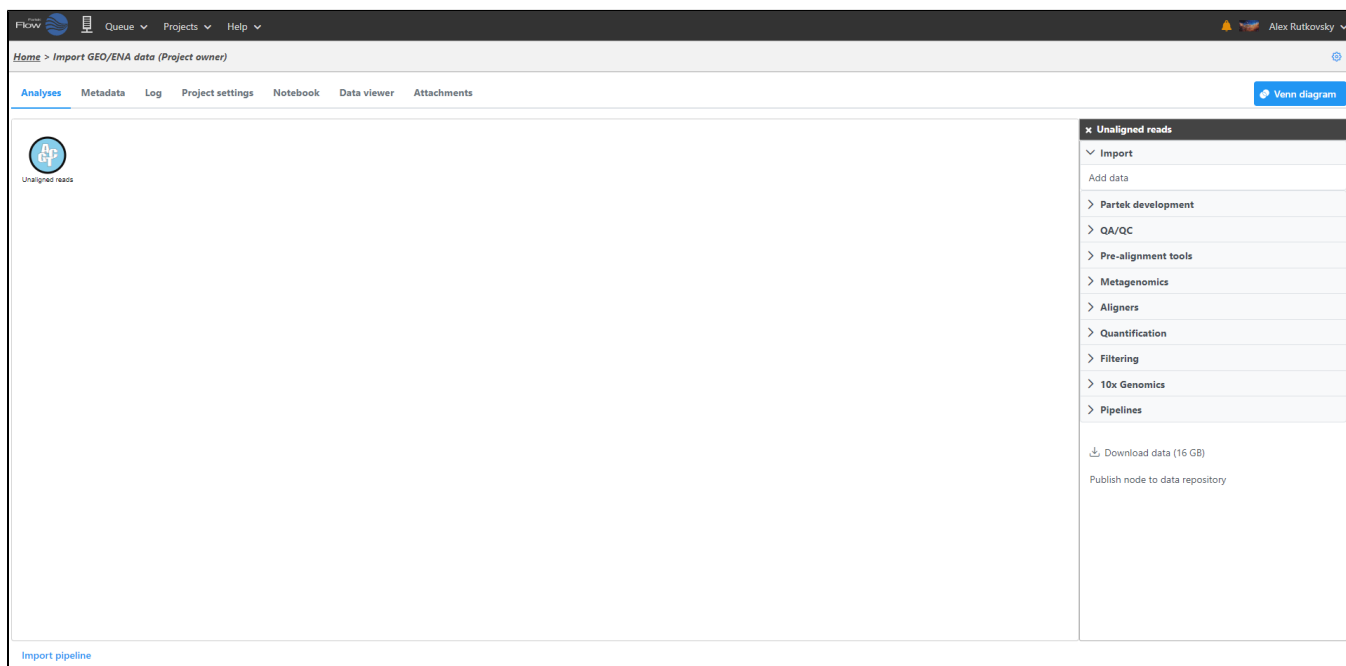


Figure 11. The Analyses tab showing a data node of unaligned reads

Data and task nodes

The Analyses tab contains two elements: data nodes (circles) and task nodes (rounded rectangles) connected by lines and arrows. Collectively, they represent a data analysis pipeline (Figure 4).

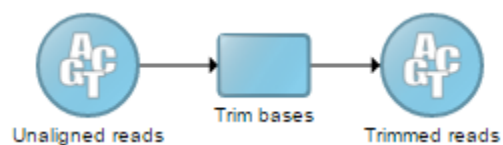


Figure 12. Example of a data analysis pipeline

Performing tasks

Clicking a data node brings up a context sensitive menu on the right (Figure 5). This menu changes depending on the type of data node. It will only present tasks which can be performed on that specific data type. Hover over the task to obtain additional information regarding each option.

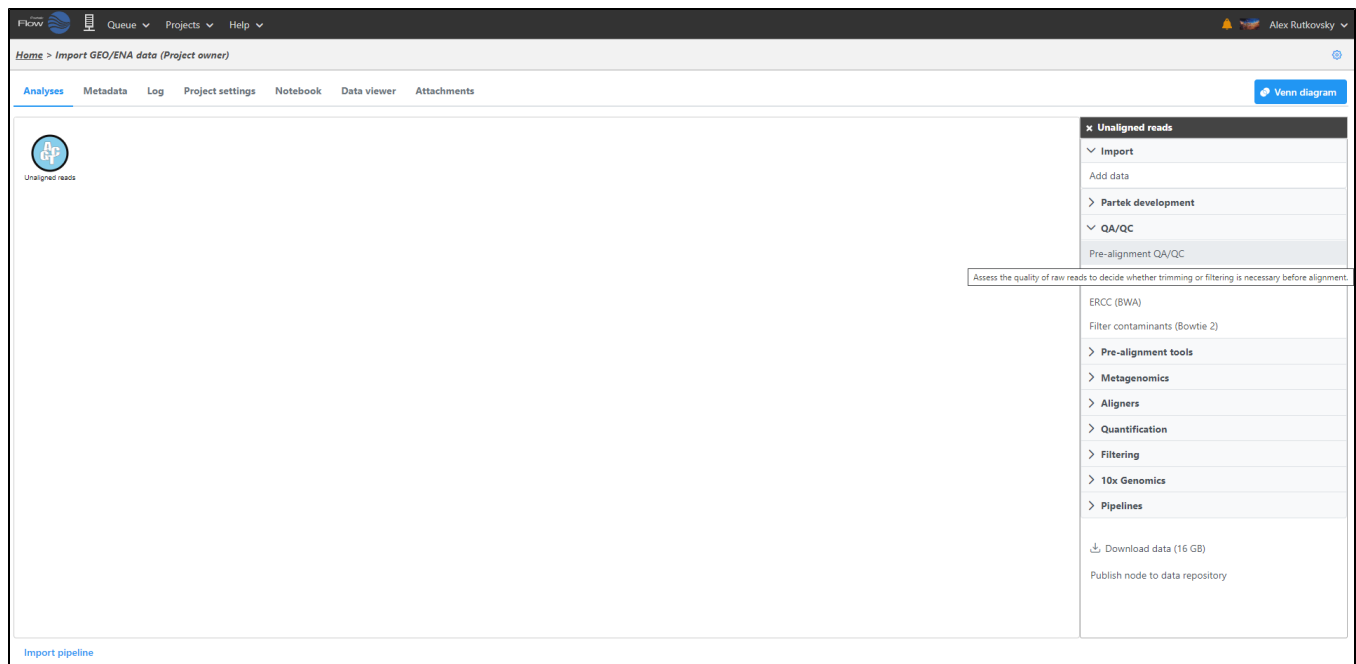


Figure 13. Context sensitive menu for unaligned reads data node

Select the task you wish to perform from the menu. When configuring task options, additional information regarding each option is available (Figure 6).

When available, hover over  Tooltips or click the  video help for decision making. Click **Finish** to perform the task.

Flow Queue Projects Help Alex Rutkovsky

Home > Liver-Muscle Demo > Trim bases

Trim mode

☒ **Quality score**
This mode scans the read from the 5' or 3' end (or both) for the first base at or above the specified quality score. All bases previous to this position are trimmed (from the left if the 5' end, from the right if the 3' end).

☐ **From 3' end**
This mode trims a certain number of bases from the 3' (right-most) end of every read.

☐ **From 5' end**
This mode trims a certain number of bases from the 5' (left-most) end of every read.

☐ **Both ends**
This mode keeps all of the bases between two points (start and stop), trimming all of the other bases from the read. When the stop point is greater than the read length, the read will keep the bases from the start point to the end of the read.

Quality trimming

End min quality level (Phred) Trim from end

Advanced options

Min read length
After trimming, discard any reads less than this length

Max N
After trimming, discards reads with larger percentage of N bases
☐ %

Quality encoding
Apply the quality encoding to all files passed to this task. Auto-detect attempts to detect and assign the correct quality type to each file.

Figure 14. Additional information about a task option

Depending on the task, a new data node may automatically be created and connected to the original data node. This contains the data resulting from the task. Tasks that do not produce new data types, such as *Pre-alignment QA/QC*, will not produce an additional data node.

To view the results of a task, click the task node and choose the **Task report** option on the menu.

Saving visualizations

Click **Save**  on any visualization to export a publication-quality image (Figure 7).

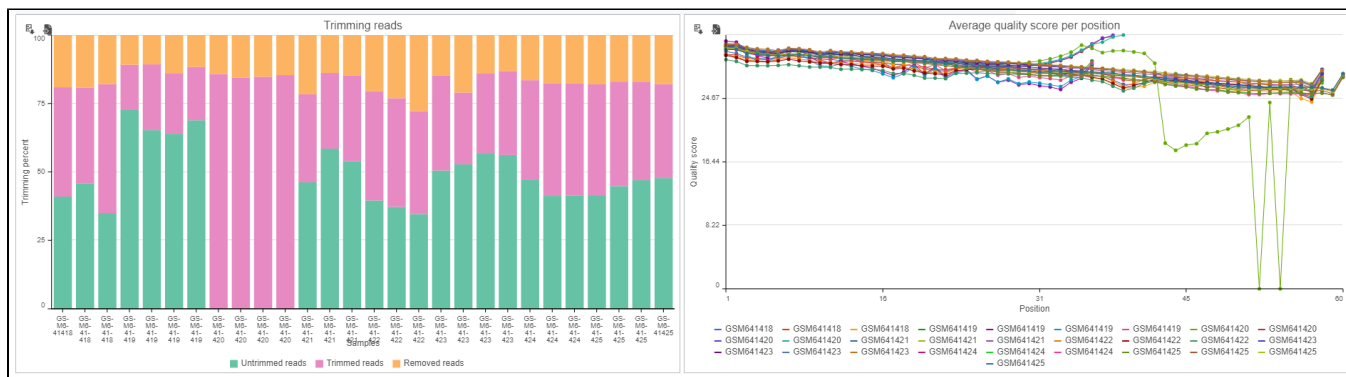


Figure 15. Save visualizations using the save icon

Downloading your data

Data associated with any data node can be downloaded by clicking the node and choosing **Download data** at the bottom of the task menu (Figure 8). Compressed files will be downloaded to the local computer where the user is accessing the Partek Flow server. Note that bigger files (such as unaligned reads) would take longer to download. For guidance, a file size estimate is provided for each data node. Downloaded files can be seamlessly imported in Partek® Genomics Suite®.

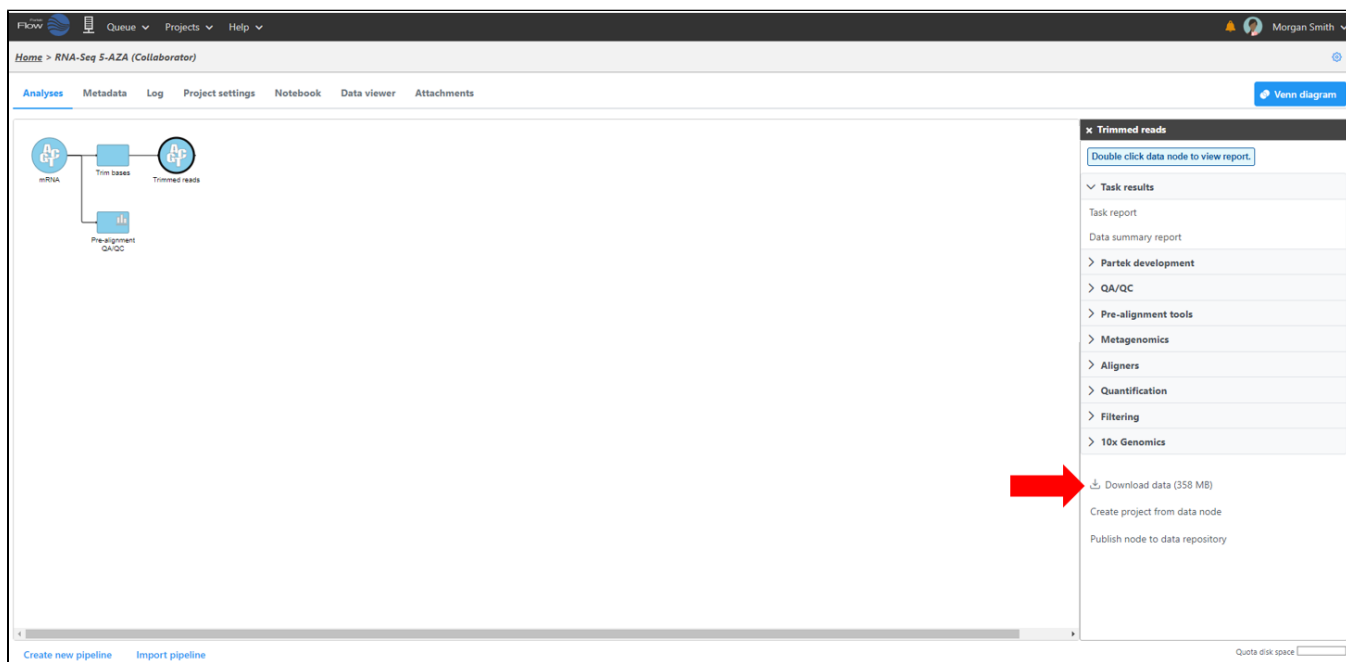


Figure 16. Downloading data

Partek Flow in action

Watch a webinar of [how to set-up a simple RNA-Seq project](#).

Additional Assistance

If you need additional assistance, please visit [our support page](#) to submit a help ticket or find phone numbers for regional support.



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